

Applicant : Hiroaki Yamamoto et al.
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REMARKS

Applicants hereby submit that the enclosures fulfill the requirements under 37 C.F.R. §1.821-1.825. Certain amendments in the specification replace the paper copy of the Sequence Listing with an amended substitute Sequence Listing wherein the general information (i.e., attorney docket number, serial number, filing date) has been updated to reflect the general information of the instant application. Additional amendments in the specification correct typographical errors (i.e., "-" to "μ"), clarify existing chemical descriptions (i.e., "chloride calcium" to "calcium chloride") or provide erroneously omitted column headings in Table 1. No new matter has been added by these amendments.

Please apply any charges or credits to Deposit Account No. 06-1050, referencing attorney docket no. 06501-092001.

Respectfully submitted,

Date:

April 16, 2002

Janis K. Fraser, Ph.D., J.D.
Reg. No. 34,819

Fish & Richardson P.C.
225 Franklin Street
Boston, Massachusetts 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

Version with markings to show changes made

In the specification:

Paragraph beginning at page 8, line 6 has been amended as follows:

Assay for the activity of oxidizing (2R,3R)-2,3-butanediol: A reaction mixture, which contains 100 mM potassium phosphate buffer (pH 8.0), 2.5 mM NADH, 50 mM (2R,3R)-2,3-butanediol and the enzyme, is allowed to react at 30°C, and the increase in absorbance at 340 nm, which is associated with the increase in the amount of NADH, is measured. 1 U is defined as the amount of enzyme capable of catalyzing 1[-]μmol increase of NADH for one minute. The quantification of polypeptide is carried out by a dye-binding method using a protein assay kit from BioRad.

Paragraph beginning on page 8, line 14 has been amended as follows:

A reaction mixture containing 100 mM potassium phosphate buffer (pH 8.0), 2.5 mM NADH, 100 mM glycerol and the enzyme is allowed to react at 30°C, and the increase in absorbance at 340 nm, which is associated with the increase in the amount of NADH, is measured. 1 U is defined as the amount of enzyme capable of catalyzing the increase of 1[-]μmol NADH for one minute.

Paragraph beginning on page 8, line 30 has been amended as follows:

The above-mentioned microorganism can be cultured in a medium that is generally used for the cultivation of fungi, such as YPD medium (medium containing 1% yeast extract, 1% peptone, and 2% glucose (pH 6.0)). To produce the (R)-2,3-butanediol dehydrogenase of the present invention, it is also possible to use YPD medium in which methanol or glycerol is substituted for glucose; a medium (pH 7.0) containing 1 g of methanol, 0.5 g of ammonium chloride, 0.1 g of potassium dihydrogen phosphate, 0.1 g of dipotassium monohydrogen phosphate, 0.05 g of magnesium sulfate heptahydrate, 3.0 mg of iron (III) chloride hexahydrate, 1.0 mg of [chloride] calcium chloride dihydrate, 1.0 mg of [chloride] manganese chloride tetrahydrate, 1.0 mg of zinc sulfate heptahydrate, 200 mg of thiamine hydrochloride and 2 mg of

biotin per 100 mL of medium (hereinafter abbreviated to medium A); and medium A in which glycerol is substituted for methanol.

Paragraph beginning on page 11, line 17 has been amended as follows:

Accordingly, in one aspect, the invention provides an isolated polynucleotide that encodes a polypeptide described herein or a fragment thereof. Preferably, the isolated [polypeptide] polynucleotide includes a nucleotide sequence that is at least 60% identical to the nucleotide sequence shown in SEQ ID NO:1. More preferably, the isolated nucleic acid molecule is at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, identical to the nucleotide sequence shown in SEQ ID NO:1. In the case of an isolated polynucleotide which is longer than or equivalent in length to the reference sequence, e.g., SEQ ID NO:1, the comparison is made with the full length of the reference sequence. Where the isolated polynucleotide is shorter than the reference sequence, e.g., shorter than SEQ ID NO:1, the comparison is made to segment of the reference sequence of the same length (excluding any loop required by the homology calculation).

Paragraph beginning on page 25, line 22 has been amended as follows:

Table 1

	<u>Protein</u>	<u>Total</u>	<u>Specific</u>	<u>Purification</u>
		<u>activity</u>	<u>activity</u>	
<i>Step</i>	<i>(mg)</i>	<i>(U)</i>	<i>(U/mg)</i>	<i>Fold</i>
Cell-free extract	2400	266	0.111	1
Blue Sepharose	884	195	0.221	2
Phenyl-Sepharose	4.0	190	47.7	431
Resource Q	0.30	66.2	218	1972